IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Baker et al.	Docket No:	39780-2830P1C47
Serial No:	10/015,671	Group Art Unit:	1647
Filed:	December 11, 2001	Examiner:	Rachel K. Hunnicutt

For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

DECLARATION OF NAPOLEONE FERRARA, Ph.D., AUDREY GODDARD, Ph.D., PAUL J. GODOWSKI, Ph.D., AUSTIN GURNEY, Ph.D., JAMES PAN, Ph.D., COLIN K. WATANABE and WILLIAM I. WOOD, Ph.D. UNDER 37 CFR 1.131

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2. We have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by U.S. Patent Publication No. 2003/0096951 (Jacobs *et al.*, publication date May 22, 2003 and effective filing date August 14, 1998).

3. The polypeptide designated as PRO1244 (SEQ ID NO:130) claimed in the above-identified application in the United States was sequenced and cloned prior to August 14, 1998.

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Audrey Goddard, Ph.D.	Date
Paul J. Godowski, Ph.D.	Date
James Pan, Ph.D.	Date
Austin Gurney, Ph.D.	Date
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10. The DNA-64883 sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 129 disclosed in the above-identified application.

11. The beginning of the cDNA sequence corresponding to SEQ ID NO: 129 in the above-identified application is shown on page 1 of the GSeqEdit database report, and the location of the first nucleotide is marked with "^insert starts here" and an arrow. The location of the last nucleotide corresponding to SEQ ID NO: 129 is shown on page 11 and is marked with an arrow.

12. The amino acid sequence shown in the GSeqEdit report is identical to that of SEQ ID NO: 130 disclosed in the above-identified application.

13. The first 26 amino acid residues of the PRO1244 polypeptide (SEQ ID NO:130) encoded by the cDNA (DNA-64883) are also shown on page 1 of the GSeqEdit report and the remaining 309 residues appear on pages 2-6 of the report.

14. All activities listed under paragraphs 4-13 were completed prior to August 14, 1998. (See Exhibit A).

15. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Napoleone Ferrara, Ph.D.	Date
Audrey Goddard, Ph.D.	Date
Paul J. Godowski, Ph.D.	Date
James Pan, Ph.D.	Date
Austin Gurney, Ph.D.	Date
Colin K. Watanabe	Date
William I. Wood, Ph.D.	10/5/04 Date

```
>[redacted]
>DNA64883 [Full]
>510 Sites [All Sites]
>[redacted] DNA64883 wiw GSeqEdit
>[redacted] DNA64883 zemin GSeqEdit
>[redacted] DNA64883 goddarda GSeqEdit
>[redacted] DNA64883 sheldens GSeqEdit
>HBN64883.seq, sequenced at ABI/ACGT by Peter Ma and Ellson Chen
>human ortholog of implantation-associated protein - Rattus

                                                          nlaIII
              mnlI                                        mslI
             taqI                                        styI
            xhoI                thaI                     ncoI
            tliI                fnuDII/mvnI              dsaI         tseI
            smlI               hinPI    aciI             btgI/bstDSI  fnu4HI/bsoFI
            paeR7I  mwoI    tseI bstUI[M.hhaI-]          bstXI        bbvI                 dde
    tsp509I[M.ecoRI-]       fnu4HI/bsoFI                 bsaJI       hinPI            taiI  bsp
   ecoRI    avaI[M.taqI-]   bbvI bsh1236I            tsp45I          hhaI/cfoI        maeII/hpyC
   apoI   mwoI bseRI    nlaIII  hhaI/cfoI         bsmAI maeIII      haeII        hpy99I   mnlI
 1 CGGAATTCGG CTCGAGGAGC GAACATGGCA GCGCGTTGGC GGTTTTGGTG TGTCTCTGTG ACCATGGTGG TGGCGCTGCT CATCGTTTGC GACGTTCCCT
   GCCTTAAGCC GAGCTCCTCG CTTGTACCGT CGCGCAACCG CCAAAACCAC ACAGAGACAC TGGTACCACC ACCGCGACGA GTAGCAAACG CTGCAAGGGA
 1                         M  A  A  R  W  R  F  W  C  V  S  V  T  M  V  V  A  L  L  I  V  C  D  V  P  S
                    ^insert starts here
                           ^MET
```

```
     mnlI                                                        aluI
    alwNI(dcm-)                                                 pvuII
    alw26I/bsmAI            bsaXI       hpy188I                 mspA1I/nspBII                                                  bsmAI
101 CAGCCTCTGC CCAAAGAAAG AAGGAGATGG TGTTATCTGA AAAGGTTAGT CAGCTGATGG AATGGACTAA CAAAAGACCT GTAATAAGAA TGAATGGAGA
    GTCGGAGACG GGTTTCTTTC TTCCTCTACC ACAATAGACT TTTCCAATCA GTCGACTACC TTACCTGATT GTTTTCTGGA CATTATTCTT ACTTACCTCT
27   A  S  A   Q  R  K   K  E  M  V   L  S  E   K  V  S   Q  L  M  E   W  T  N   K  R  P   V  I  R  M   N  G  D

                                                                 tspRI                bst4CI/hpyCH4III    cac8I
                                                                 btsI                ahdI/eam1105I    cac8I
        hpy99I                              tsp509I              nlaIII              hpyCH4V tspRI        hpyCH4V al
201 CAAGTTCCGT CGCCTTGTGA AAGCCCCACC GAGAAATTAC TCCGTTATCG TCATGTTCAC TGCTCTCCAA CTGCATAGAC AGTGTGTCGT TTGCAAGCAA
    GTTCAAGGCA GCGGAACACT TTCGGGGTGG CTCTTTAATG AGGCAATAGC AGTACAAGTG ACGAGAGGTT GACGTATCTG TCACACAGCA AACGTTCGTT
60   K  F  R   R  L  V  K   A  P  P   R  N  Y   S  V  I  V   M  F  T   A  L  Q   L  H  R  Q   C  V  V   C  K  Q
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```
                    scrFI[dcm-]
                    pspGI
                    mvaI
                    ecoRII[dcm-]
                    dsaV[dcm-]
                    bstNI
                    bssKI[dcm-]
                    apyI[dcm+]
                sau3AI
                mboI/ndeII[dam-]
                dpnII[dam-]
                dpnI[dam+]
                alwI[dam-]        scrFI[dcm-]
               bstYI/xhoII        pspGI
              alwNI[dcm-]         mvaI                                               nlaIII
              alw26I/bsmAI        ecoRII[dcm-]                                       styI
         tsp509I[M.ecoRI-]        dsaV[dcm-]       hpyCH4V                           ncoI
       ecoRI pflMI[dcm-]          bstNI baeI    tspRI                                dsaI
       apoI  bslI[dcm-]           bssKI[dcm-]  bsrI bsmI hphI                        btgI/bstDSI
    mboII   hpy188III             apyI[dcm+] bpmI/gsuI[dcm-]                         bsaJI                      hpy18
301 GCTGATGAAG AATTCCAGAT CCTGGCAAAC TCCTGGCGAT ACTCCAGTGC ATTCACCAAC AGGATATTTT TTGCCATGGT GGATTTTGAT GAAGGCTCTG
    CGACTACTTC TTAAGGTCTA GGACCGTTTG AGGACCGCTA TGAGGTCACG TAAGTGGTTG TCCTATAAAA AACGGTACCA CCTAAAACTA CTTCCGAGAC
 93 A  D  E  E   F  Q  I   L  A  N   S  W  R  Y   S  S  A   F  T  N   R  I  F  F   A  M  V   D  F  D   E  G  S  D
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```
                          tsp509I[M.ecoRI-]
                          ecoRI                                   hpyCH4V
              sfaNI       apoI                                    ecoNI
          hpy188I    nlaIII     aluI                              bslI        bslI       hphI     ndeI    maeIII    aciI
401 ATGTATTTCA GATGCTAAAC ATGAATTCAG CTCCAACTTT CATCAACTTT CCTGCAAAAG GGAAACCCAA ACGGGGTGAT ACATATGAGT TACAGGTGCG
    TACATAAAGT CTACGATTTG TACTTAAGTC GAGGTTGAAA GTAGTTGAAA GGACGTTTTC CCTTTGGGTT TGCCCCACTA TGTATACTCA ATGTCCACGC
127  V  F  Q   M  L  N   M  N  S  A   P  T  F   I  N  F   P  A  K  G   K  P  K   R  G  D   T  Y  E  L   Q  V  R

               ddeI[M.aluI-]
               bspCNI         mspI     sau3AI
              celII/espI      hpaII    mboI/ndeII[dam-]
              blpI/bpu1102I scrFI[M.hpaII-]                                                                bsmFI
            aluI              nciI     dpnII[dam-]                                                        sau96I
           pvuII              dsaV     dpnI[dam+]                                                         nlaIV
           mspA1I/nspBII      bssKI alwI[dam-]                    sspI                         tsp509I    avaII bslI
501 GGGTTTTTCA GCTGAGCAGA TTGCCCGGTG GATCGCCGAC AGAACTGATG TCAATATTAG AGTGATTAGA CCCCCAAATT ATGCTGGTCC CCTTATGTTG
    CCCAAAAAGT CGACTCGTCT AACGGGCCAC CTAGCGGCTG TCTTGACTAC AGTTATAATC TCACTAATCT GGGGGTTTAA TACGACCAGG GGAATACAAC
160  G  F  S   A  E  Q  I   A  R  W   I  A  D   R  T  D  V   N  I  R   V  I  R   P  P  N  Y   A  G  P   L  M  L

                                         taqI                                                         aluI
                                         sfuI                                                         tseI
                                         bstBI                                        fokI           fnu4HI/bsoFI
                                         bsiCI                tsp509I   tru9I         bstF5I         bbvI
                                baeI    mboII mboII           apoI      mseI      bsrI       mwoI hpyCH4V
601 GGATTGCTTT TGGCTGTTAT TGGTGGACTT GTGTATCTTC GAAGAAGTAA TATGGAATTT CTCTTTAATA AAACTGGATG GGCTTTTGCA GCTTTGTGTT
    CCTAACGAAA ACCGACAATA ACCACCTGAA CACATAGAAG CTTCTTCATT ATACCTTAAA GAGAAATTAT TTTGACCTAC CCGAAAACGT CGAAACACAA
193 G  L  L  L   A  V  I   G  G  L   V  Y  L  R   R  S  N   M  E  F   L  F  N  K   T  G  W   A  F  A   A  L  C  F
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                                                                                    nlaIII          nlaIII
                                                                                   pciI            styI
                                                                                   nspHI           ncoI
                                                 sau96I                bslI        nspI            dsaI
                                                 avaII             tfiI            aflIII          btgI/bs
        cac8I     ahdI/eam1105I     nlaIV        mnlI      ndeI    hinfI       bsmFI      tsp509I  bsaJI
701 TTGTGCTTGC TATGACATCT GGTCAAATGT GGAACCATAT AAGAGGACCA CCATATGCCC ATAAGAATCC CCACACGGGA CATGTGAATT ATATCCATGG
    AACACGAACG ATACTGTAGA CCAGTTTACA CCTTGGTATA TTCTCCTGGT GGTATACGGG TATTCTTAGG GGTGTGCCCT GTACACTTAA TATAGGTACC
227  V  L  A   M  T  S   G  Q  M  W   N  H  I   R  G  P   P  Y  A  H   K  N  P   H  T  G   H  V  N  Y   I  H  G

                                                                 ddeI                         tseI
                                                                 eco81I                       fnu4HI/bsoFI
                                                     tru9I       bsu36I/mstII/sauI            bbvI      hpy1
               bsrI      aluI             mboII      mseI      maeIII                        aluI      mnlI
801 AAGCAGTCAA GCCCAGTTTG TAGCTGAAAC ACACATTGTT CTTCTGTTTA ATGGTGGAGT TACCTTAGGA ATGGTGCTTT TATGTGAAGC TGCTACCTCT
    TTCGTCAGTT CGGGTCAAAC ATCGACTTTG TGTGTAACAA GAAGACAAAT TACCACCTCA ATGGAATCCT TACCACGAAA ATACACTTCG ACGATGGAGA
260 S  S  Q   A  Q  F  V   A  E  T   H  I  V   L  L  F  N   G  G  V   T  L  G   M  V  L  L   C  E  A   A  T  S

                                                                                              sau3AI
                                                                                              mboI/ndeII[dam
                                                                                              dpnII[dam-]
                                                                          sfaNI               dpnI[dam+]
                                                                 eco57I   fokI                bstYI/xhoII
      nlaIII                                                     mboII    bstF5I              bglII      nl
901 GACATGGATA TTGGAAAGCG AAAGATAATG TGTGTGGCTG GTATTGGACT TGTTGTATTA TTCTTCAGTT GGATGCTCTC TATTTTTAGA TCTAAATATC
    CTGTACCTAT AACCTTTCGC TTTCTATTAC ACACACCGAC CATAACCTGA ACAACATAAT AAGAAGTCAA CCTACGAGAG ATAAAAATCT AGATTTATAG
293 D  M  D  I   G  K  R   K  I  M   C  V  A  G   I  G  L   V  V  L   F  F  S  W   M  L  S   I  F  R   S  K  Y  H
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                                  bsmFI
                                  sau96I                          bsrI
                                  nlaIV                         rsaI
                                  avaII                      bpmI/gsuI[dcm-]
                             tru9I  ppuMI                    bsrI   csp6I
                 aluI hpy188I    mseI   eco0109I/draII        tspRI   scaI     tsp509I
1001 ATGGCTACCC ATACAGCTTT CTGATGAGTT AAAAAGGTCC CAGAGATATA TAGACACTGG AGTACTGGAA ATTGAAAAAC GAAAATCGTG TGTGTTTGAA
     TACCGATGGG TATGTCGAAA GACTACTCAA TTTTTCCAGG GTCTCTATAT ATCTGTGACC TCATGACCTT TAACTTTTTG CTTTTAGCAC ACACAAACTT
327   G  Y  P  Y  S  F  L  M  S  O

                                                       tru9I
                                                       mseI    tru9I
       bsmI                                        ahaIII/draI      tru9I                      tru9I
     mboII hpyCH4V                  mnlI            swaI      mseI      mseI     mboII          mseI
1101 AAGAAGAATG CAACTTGTAT ATTTTGTATT ACCTCTTTTT TTCAAGTGAT TTAAATAGTT AATCATTTAA CCAAAGAAGA TGTGTAGTGC CTTAACAAGC
     TTCTTCTTAC GTTGAACATA TAAAACATAA TGGAGAAAAA AAGTTCACTA AATTTATCAA TTAGTAAATT GGTTTCTTCT ACACATCACG GAATTGTTCG

                 mnlI
                ddeI                                  bsrI                       tsp509I      tru9I
                bspCNI                 mnlI tru9I    mboII tspRI               tru9I     rsaI tsp509I
       mnlI     hpy188I            tsp509I   mseI   earI/ksp632I               mseI     csp6I  mseI
1201 AATCCTCTGT CAAAATCTGA GGTATTTGAA AATAATTATC CTCTTAACCT TCTCTTCCCA GTGAACTTTA TGGAACATTT AATTTAGTAC AATTAAGTAT
     TTAGGAGACA GTTTTAGACT CCATAAACTT TTATTAATAG GAGAATTGGA AGAGAAGGGT CACTTGAAAT ACCTTGTAAA TTAAATCATG TTAATTCATA

                                                                   tru9I
                                                                   mseI
                                                                  hpaI
      psiI   tsp509I                       aluI                   hincII/hindII hpy188I                bslI
1301 ATTATAAAAA TTGTAAAACT ACTACTTTGT TTTAGTTAGA ACAAAGCTCA AAACTACTTT AGTTAACTTG GTCATCTGAT TTTATATTGC CTTATCCAAA
     TAATATTTTT AACATTTTGA TGATGAAACA AAATCAATCT TGTTTCGAGT TTTGATGAAA TCAATTGAAC CAGTAGACTA AAATATAACG GAATAGGTTT
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                                scrFI[dcm-]
                                pspGI
                                mvaI
                                ecoRII[dcm-]
                                dsaV[dcm-]
                                bstNI                                   tsp509I[M.ecoRI-]
                                bssKI[dcm-]                             xmnI
                                apyI[dcm+]                              ecoRI           mboII
                               sexAI                                    asp700      aluI    mslI        fokI
                        hpy188III          ndeI     maeIII              apoI     ddeI[M.aluI-]          bstF5I
1401 GATGGGGAAA GTAAGTCCTG ACCAGGTGTT CCCACATATG CCTGTTACAG ATAACTACAT TAGGAATTCA TTCTTAGCTT CTTCATCTTT GTGTGGATGT
     CTACCCCTTT CATTCAGGAC TGGTCCACAA GGGTGTATAC GGACAATGTC TATTGATGTA ATCCTTAAGT AAGAATCGAA GAAGTAGAAA CACACCTACA

                                                                                                  taiI
                                                                                              hgiAI/aspHI
                                                                                              bsp1286
                                                                    hpy188I                   bsiHKAI    rmaI  ddeI
     bstZ17I                                                        mboII                   hpy188I   maeII/hpyCH4IV
     bst1107I                                                       bpuAI                  eco57I    aflIII maeI  bspC
     accI        sfaNI                       tsp509I      nlaIII bbsI                    mboII  bmyI btrI  bfaI mnlI
1501 GTATACTTTA CGCATCTTTC CTTTTGAGTA GAGAAATTAT GTGTGTCATG TGGTCTTCTG AAAATGGAAC ACCATTCTTC AGAGCACACG TCTAGCCCTC
     CATATGAAAT GCGTAGAAAG GAAAACTCAT CTCTTTAATA CACACAGTAC ACCAGAAGAC TTTTACCTTG TGGTAAGAAG TCTCGTGTGC AGATCGGGAG
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                                                                                tth111I/aspI
                                                                                pleI
                    bseRI                                                       pflFI
                   mnlI                               bpmI/gsuI[dcm-]           mlyI
                 bseRI                              hinPI       ddeI            hinfI
        bst4CI/hpyCH4III mnlI  hpyCH4V              hhaI/cfoI   bspCNI        bsmAI     bsmAI
1601 AGCAAGACAG TTGTTTCTCC TCCTCCTTGC ATATTTCCTA CTGCGCTCCA GCCTGAGTGA TAGAGTGAGA CTCTGTCTCA AAAAAAAGTA TCTCTAAATA
     TCGTTCTGTC AACAAAGAGG AGGAGGAACG TATAAAGGAT GACGCGAGGT CGGACTCACT ATCTCACTCT GAGACAGAGT TTTTTTTCAT AGAGATTTAT

                                  tru9I                                                                tsp45I
                                  mseI                          tfiI                                  hphI
            tsp509I             hpaI               xmnI         hinfI                              tru9I maeIII
       psiI        smlI         hincII/hindII      asp700    hpy188I           ddeI                mseI bstEII
1701 CAGGATTATA ATTTCTGCTT GAGTATGGTG TTAACTACCT TGTATTTAGA AAGATTTCAG ATTCATTCCA TCTCCTTAGT TTTCTTTTAA GGTGACCCAT
     GTCCTAATAT TAAAGACGAA CTCATACCAC AATTGATGGA ACATAAATCT TTCTAAAGTC TAAGTAAGGT AGAGGAATCA AAAGAAAATT CCACTGGGTA

                                                                                                          dde
                   ddeI[M.aluI-]       maeIII        haeIII/palI                       tsp45I          rsaI
                 aluI              tspRI         nlaIII                     tsp509I   maeIII          csp6I
1801 CTGTGATAAA AATATAGCTT AGTGCTAAAA TCAGTGTAAC TTATACATGG CCTAAAATGT TTCTACAAAT TAGAGTTTGT CACTTATTCC ATTTGTACCT
     GACACTATTT TTATATCGAA TCACGATTTT AGTCACATTG AATATGTACC GGATTTTACA AAGATGTTTA ATCTCAAACA GTGAATAAGG TAAACATGGA
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```
                                       scrFI[dcm-]
                                       pspGI
                                       mvaI
                                       ecoRII[dcm-]
                                       dsaV[dcm-]
                                       bstNI
                                     haeIII/palI
                                    mscI/balI[dcm-]
                                    eaeI[dcm-]
                                    cfrI
                                  scrFI[dcm-]
                                  pspGI
                                  mvaI bssKI[dcm-]
                                  ecoRII[dcm-]   tsp45I
                                  dsaV[dcm-]     maeIII                                          bssS
                                  bstNI     hinPI                                                  hpy18
                                  bssKI[dcm-]  tspRI                                              sau3AI
                            pleI bslI[dcm-] hhaI/cfoI                                 styI cac8I  mboI/nd
              ddeI          mlyI bsaJI apyI[dcm+]                 ddeI              haeIII/palI   dpnII[d
              bspCNI        hinfI apyI[dcm+]  btsI                bspCNI        mnlI bsaJI        dpnI[da
1901 AAGAGAAAAA TAGGCTCAGT TAGAAAAGGA CTCCCTGGCC AGGCGCAGTG ACTTACGCCT GTAATCTCAG CACTTTGGGA GGCCAAGGCA GGCAGATCAC
     TTCTCTTTTT ATCCGAGTCA ATCTTTTCCT GAGGGACCGG TCCGCGTCAC TGAATGCGGA CATTAGAGTC GTGAAACCCT CCGGTTCCGT CCGTCTAGTG
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                                  mscI/ball[dcm-]
                                  eaeI[dcm-]
                                 scrFI[dcm-]
                                 pspGI
                                 mvaI
                                 ecoRII[dcm-]
                                 dsaV[dcm-]
                                 bstNI
                      bsmAI      bssKI[dcm-]
                     taqI   fokI  cfrI    nlaIII         bsmAI
          hpy188III  bsaI bstF5I haeIII/palI          esp3I                    aluI
    mnlI          hpy188III  apyI[dcm+]   hphI       bsmBI                tsp509I              nlaIV
2001 GAGGTCAGGA GTTCGAGACC ATCCTGGCCA ACATGGTGAA ACCCCGTCTC TACTAAAAAT ATAAAAATTA GCTGGGTGTG GTGGCAGGAG CCTGTAATCC
     CTCCAGTCCT CAAGCTCTGG TAGGACCGGT TGTACCACTT TGGGGCAGAG ATGATTTTTA TATTTTTAAT CGACCCACAC CACCGTCCTC GGACATTAGG

                                                                                                    scrFI[dcm-]
                                                                                                    pspGI
                                                                                                    mvaI
                                                                                                    ecoRII[dcm-]
                                                                                  tspRI             dsaV[dcm-]
                                                                              sau3AI   btsI         bstNI
                      ddeI        tfiI          hpy188III                     mboI/ndeII[dam-]      bssKI[dcm-]
                      bspCNI      hinfI        ddeI                           dpnII[dam-] hpyCH4V   apyI[dcm+]
     aluI       mnlI  mnlI bssSI              bspCNI      mnlI    tspRI      dpnI[dam+] bsgI  bpmI/gsuI[dcm-]
2101 CAGCTACACA GGAGGCTGAG GCACGAGAAT CACTTGAACT CAGGAGATGG AGGTTTCAGT GAGCCGAGAT CACGCCACTG CACTCCAGCC TGGCAACAGA
     GTCGATGTGT CCTCCGACTC CGTGCTCTTA GTGAACTTGA GTCCTCTACC TCCAAAGTCA CTCGGCTCTA GTGCGGTGAC GTGAGGTCGG ACCGTTGTCT
```

```
                                                        fnu4HI/bsoFI
                                                       haeIII/palI
                                                      mcrI
                                                      eagI/xmaIII/eclXI
                                                      eaeI
                                                      cfrI
          pleI                                        bsiEI      xmaI
          mlyI                                      notI         maeI
          hinfI                                     fnu4HI/bsoFI bfaI
        bsmAI                                       aciI aciI  speI
2201 GCGAGACTCC ATCTCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAGGG CGGCCGCCGA CTAGTGAGC
     CGCTCTGAGG TAGAGTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTCCC GCCGGCGGCT GATCACTCG
```

> length: 2269

accI(GTMKAC):	1501
aciI(CCGC):	39 498 2250 2254
aflIII(ACRYGT):	780 1586
ahaIII(TTTAAA):	1150
ahdI(GACNNNNNGTC):	278 714
aluI(AGCT):	152 300 429 510 690 822 888 1015 1345 1476 1816 2070 2102
alw26I(CAGNNNCTG):	101 316
alwI(GGATCNNNN):	318 530
alwNI(CAGNNNCTG):	101 316
apoI(RAATTY):	3 310 423 655 1464
apyI(CCWGG):	321 332 1422 1934 1939 2023 2189
asp700(GAANNNNTTC):	1464 1749
aspHI(GWGCWC):	1582